

SEQUENCE LISTING



ATTACHMENT
- A -

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Kim, Kyung Jin

<120> DR4 ANTIBODIES AND USES THEREOF

<130> 11669.19US02

<140> 09/237,299

<141> 1999-01-25

<150> 60/072,481

<151> 1998-01-26

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 1407

<212> DNA

<213> Homo sapiens

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<222> (1)..(1407)

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act ccg aat ccc ggg agc gca gcg agt ggg aca gag gca gcc gcg gcc	96
Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr Glu Ala Ala Ala Ala	
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aca ccc agc aaa gtg tgg ggc tct tcc gcg ggg agg att gaa cca cga	144
Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg	
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ggc ggg ggc cga gga gcg ctc cct acc tcc atg gga cag cac gga ccc	192
Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro	
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agt gcc cgg gcc cgg gca ggg cgc gcc cca gga ccc agg ccg gcg cgg	240
Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg	
65 70 75 80	

gaa gcc agc cct cgg ctc cgg gtc cac aag acc ttc aag ttt gtc gtc	288
Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val Val	
85 90 95	
gtc ggg gtc ctg ctg cag gtc gta cct agc tca gct gca acc atc aaa	336
Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr Ile Lys	
100 105 110	
ctt cat gat caa tca att ggc aca cag caa tgg gaa cat agc cct ttg	384
Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu	
115 120 125	
gga gag ttg tgt cca cca gga tct cat aga tca gaa cgt cct gga gcc	432
Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu Arg Pro Gly Ala	
130 135 140	
tgt aac cgg tgc aca gag ggt gtg ggt tac acc aat gct tcc aac aat	480
Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn	
145 150 155 160	
ttg ttt gct tgc ctc cca tgt aca gct tgt aaa tca gat gaa gaa gag	528
Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys Ser Asp Glu Glu Glu	
165 170 175	
aga agt ccc tgc acc acg acc agg aac aca gca tgt cag tgc aaa cca	576
Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala Cys Gln Cys Lys Pro	
180 185 190	
gga act ttc cgg aat gac aat tct gct gag atg tgc cgg aag tgc agc	624
Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met Cys Arg Lys Cys Ser	
195 200 205	
aca ggg tgc ccc aga ggg atg gtc aag gtc aag gat tgt acg ccc tgg	672
Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys Asp Cys Thr Pro Trp	
210 215 220	
agt gac atc gag tgt gtc cac aaa gaa tca ggc aat gga cat aat ata	720
Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Asn Gly His Asn Ile	
225 230 235 240	
tgg gtg att ttg gtt gtg act ttg gtt gtt ccg ttg ctg ttg gtg gct	768
Trp Val Ile Leu Val Val Thr Leu Val Val Pro Leu Leu Leu Val Ala	
245 250 255	
gtg ctg att gtc tgt tgt tgc atc ggc tca ggt tgt gga ggg gac ccc	816
Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly Cys Gly Gly Asp Pro	
260 265 270	

aag tgc atg gac agg gtg tgt ttc tgg cgc ttg ggt ctc cta cga ggg	864
Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu Gly Leu Leu Arg Gly	
275 280 285	
cct ggg gct gag gac aat gct cac aac gag att ctg agc aac gca gac	912
Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile Leu Ser Asn Ala Asp	
290 295 300	
tcg ctg tcc act ttc gtc tct gag cag caa atg gaa agc cag gag ccg	960
Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met Glu Ser Gln Glu Pro	
305 310 315 320	
gca gat ttg aca ggt gtc act gta cag tcc cca ggg gag gca cag tgt	1008
Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro Gly Glu Ala Gln Cys	
325 330 335	
ctg ctg gga ccg gca gaa gct gaa ggg tct cag agg agg agg ctg ctg	1056
Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln Arg Arg Arg Leu Leu	
340 345 350	
gtt cca gca aat ggt gct gac ccc act gag act ctg atg ctg ttc ttt	1104
Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr Leu Met Leu Phe Phe	
355 360 365	
gac aag ttt gca aac atc gtg ccc ttt gac tcc tgg gac cag ctc atg	1152
Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met	
370 375 380	
agg cag ctg gac ctc acg aaa aat gag atc gat gtg gtc aga gct ggt	1200
Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly	
385 390 395 400	
aca gca ggc cca ggg gat gcc ttg tat gca atg ctg atg aaa tgg gtc	1248
Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp Val	
405 410 415	
aac aaa act gga cgg aac gcc tcg atc cac acc ctg ctg gat gcc ttg	1296
Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu	
420 425 430	
gag agg atg gaa gag aga cat gca aaa gag aag att cag gac ctc ttg	1344
Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp Leu Leu	
435 440 445	
gtg gac tct gga aag ttc atc tac tta gaa gat ggc aca ggc tct gcc	1392
Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu Asp Gly Thr Gly Ser Ala	
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Val Ser Leu Glu
465

1407

<210> 2
<211> 468
<212> PRT
<213> Homo sapiens

<400> 2
Met Ala Pro Pro Pro Ala Arg Val His Leu Gly Ala Phe Leu Ala Val
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Thr Pro Asn Pro Gly Ser Ala Ala Ser Gly Thr Glu Ala Ala Ala Ala
20 25 30

Thr Pro Ser Lys Val Trp Gly Ser Ser Ala Gly Arg Ile Glu Pro Arg
35 40 45

Gly Gly Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro
50 55 60

Ser Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg
65 70 75 80

Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val Val
85 90 95

Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr Ile Lys
100 105 110

Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His Ser Pro Leu
115 120 125

Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu Arg Pro Gly Ala
130 135 140

Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr Asn Ala Ser Asn Asn
145 150 155 160

Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys Lys Ser Asp Glu Glu Glu
165 170 175

Arg Ser Pro Cys Thr Thr Thr Arg Asn Thr Ala Cys Gln Cys Lys Pro
180 185 190

Gly Thr Phe Arg Asn Asp Asn Ser Ala Glu Met Cys Arg Lys Cys Ser	195	200	205
Thr Gly Cys Pro Arg Gly Met Val Lys Val Lys Asp Cys Thr Pro Trp	210	215	220
Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Asn Gly His Asn Ile	225	230	235 240
Trp Val Ile Leu Val Val Thr Leu Val Val Pro Leu Leu Leu Val Ala	245	250	255
Val Leu Ile Val Cys Cys Cys Ile Gly Ser Gly Cys Gly Gly Asp Pro	260	265	270
Lys Cys Met Asp Arg Val Cys Phe Trp Arg Leu Gly Leu Leu Arg Gly	275	280	285
Pro Gly Ala Glu Asp Asn Ala His Asn Glu Ile Leu Ser Asn Ala Asp	290	295	300
Ser Leu Ser Thr Phe Val Ser Glu Gln Gln Met Glu Ser Gln Glu Pro	305	310	315 320
Ala Asp Leu Thr Gly Val Thr Val Gln Ser Pro Gly Glu Ala Gln Cys	325	330	335
Leu Leu Gly Pro Ala Glu Ala Glu Gly Ser Gln Arg Arg Arg Leu Leu	340	345	350
Val Pro Ala Asn Gly Ala Asp Pro Thr Glu Thr Leu Met Leu Phe Phe	355	360	365
Asp Lys Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met	370	375	380
Arg Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly	385	390	395 400
Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp Val	405	410	415
Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp Ala Leu	420	425	430
Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln Asp Leu Leu	435	440	445

Val Asp Ser Gly Lys Phe Ile Tyr Leu Glu Asp Gly Thr Gly Ser Ala
450 455 460

Val Ser Leu Glu
465